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### Permalink

<https://escholarship.org/uc/item/0cj8t9rv>

### Journal

Genome announcements, 2(6)

### ISSN

2169-8287

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### Publication Date

2014-11-01

### DOI

10.1128/genomea.00977-14

Peer reviewed

# Genome Sequence of *Corynebacterium pseudotuberculosis* MB20 bv. equi Isolated from a Pectoral Abscess of an Oldenburg Horse in California

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**The genome of *Corynebacterium pseudotuberculosis* MB20 bv. equi was sequenced using the Ion Personal Genome Machine (PGM) platform, and showed a size of 2,363,089 bp, with 2,365 coding sequences and a GC content of 52.1%. These results will serve as a basis for further studies on the pathogenicity of *C. pseudotuberculosis* bv. equi.**

Received 28 August 2014 Accepted 8 October 2014 Published 13 November 2014

**Citation** Baraúna RA, Guimarães LC, Veras AAO, de Sá PHCG, Graças DA, Pinheiro KC, Silva ASS, Folador EL, Benevides LJ, Viana MVC, Carneiro AR, Schneider MPC, Spier SJ, Edman JM, Ramos RTJ, Azevedo V, Silva A. 2014. Genome sequence of *Corynebacterium pseudotuberculosis* MB20 bv. equi isolated from a pectoral abscess of an Oldenburg horse in California. *Genome Announc.* 2(6):e00977-14. doi:10.1128/genomeA.00977-14.

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Recent advances have been made in the genomic analysis of *Corynebacterium pseudotuberculosis*, a species of veterinary and biotechnological interest. Molecular diagnosis of several diseases caused by this species was achieved using multiplex PCR (PCR) (1), and a description of its pangenome was published using 15 strains of *C. pseudotuberculosis* bv. ovis and equi (2). *C. pseudotuberculosis* bv. equi comprises strains that infect horses and cattle and cause infection of cutaneous lymphatic vessels, termed ulcerative lymphangitis, which is characterized by the development of multiple waxy ulcerative lesions. The incidence of this disease in horses has been reported in the literature since the 1910s (3) and remains prevalent in animals worldwide (4, 5); moreover, this infection is likely underreported and has been characterized as a neglected zoonosis (6).

The host-pathogen interaction in this disease has been studied using omics approaches (7). For instance, the differential gene expression of a *C. pseudotuberculosis* bv. ovis strain was analyzed using RNA-seq, and genes involved in the molecular responses of the bacterium to different stresses during infection were identified (8). A study of reverse vaccinology reported by Soares et al. (9) identified 49 possible antigens from the genome of the *C. pseudotuberculosis* bv. equi strain 258 that may serve as targets for the development of effective vaccines. In addition, a new *C. pseudotuberculosis* bv. equi strain was isolated and sequenced, which will aid in future broader studies. These new data combined with those already reported will serve as a basis for the development of studies aimed at a better understanding of the pathogenic potential of *C. pseudotuberculosis* bv. equi.

The MB20 strain was isolated from a pectoral abscess of a 4-year-old horse of the breed Oldenburg, raised in the city of Vacaville, CA, USA. Genomic DNA was sequenced from a fragment library on a 318 chip of the Ion Torrent Personal Genome Machine (PGM) platform (Life Technologies). A total of 2,331,864 reads were

generated with an average length of 420 bp, which were used for genome assembly using the software Mira (10). The contigs generated with Mira were analyzed using the SeqMan Pro tool of the software Lasergene 11 Core Suite (DNASTAR) to remove redundant sequences. This approach resulted in 3 contigs, which were sorted with the Artemis Comparison tool (11) using the genome of *C. pseudotuberculosis* 316 as a reference. The scaffold produced at the end of the assembly was 2,363,089 bp in size and underwent automatic annotation using Rapid Annotation using Subsystem Technology (RAST) (12). As a result, 2,365 coding sequences (CDSs), 11 rRNA genes, 51 tRNA genes and a 52.1% GC content were identified. Of the 2,365 CDSs, 790 (33.4%) were classified as hypothetical proteins.

**Nucleotide sequence accession numbers.** The genomic sequence obtained in this study was deposited in the DDBJ/EMBL/GenBank under accession number [JPUV000000000](https://www.ncbi.nlm.nih.gov/nuccore/JPUV000000000). The version described in this paper is version JPUV01000000.

## ACKNOWLEDGMENTS

This study was conducted by the Rede Paraense de Genômica e Proteômica, with support from the Conselho Nacional de Desenvolvimento Científico e Tecnológico (CNPq), the Coordenação de Aperfeiçoamento de Pessoal de Nível Superior (CAPES), and the Fundação de Amparo a Pesquisa do Estado do Pará (FAPESPA).

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